

SEQUENCE LISTING

<110> Kloek, Andrew
Williams, Deryck Jeremy
Salmon, Brandy

<120> NEMATODE GS-LIKE SEQUENCES

<130> 12557-004001

<150> US 60/276,621

<151> 2001-03-16

<160> 9

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1471

<212> DNA

<213> Meloidogyne incognita

<220>

<221> CDS

<222> (34)...(1395)

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cta aat aat ttg att aga aat gga aaa att gac acg gta gtt ttg gca	102
Leu Asn Asn Leu Ile Arg Asn Gly Lys Ile Asp Thr Val Val Leu Ala	
10 15 20	
tgc gtc gac atg caa ggc cgg ctg atg ggc aag aga tta act ggg cgt	150
Cys Val Asp Met Gln Gly Arg Leu Met Gly Lys Arg Leu Thr Gly Arg	
25 30 35	
cat ttt tta gga ttg gat caa aag aag att agc att agc acg ttt gta	198
His Phe Leu Gly Leu Asp Gln Lys Lys Ile Ser Ile Ser Thr Phe Val	
40 45 50 55	
tat gcg gta act ata gaa ggc atc gct ggc gga ggt tat gag atc tca	246
Tyr Ala Val Thr Ile Glu Gly Ile Ala Gly Gly Gly Tyr Glu Ile Ser	
60 65 70	
agt gta gac aca ggt tat agt gat tgt cat ctc tgt gca gat ttg aat	294
Ser Val Asp Thr Gly Tyr Ser Asp Cys His Leu Cys Ala Asp Leu Asn	
75 80 85	
tcc ctt cat tta ctc ccg tgg tca gaa ggc gct gta ttg gca att tcc	342
Ser Leu His Leu Leu Pro Trp Ser Glu Gly Ala Val Leu Ala Ile Ser	
90 95 100	

aat cct cat aat ttc gtt act tct gag cca ttg ttc tgt tct cct cga Asn Pro His Asn Phe Val Thr Ser Glu Pro Leu Phe Cys Ser Pro Arg 105 110 115	390
gta ata ctc atg cag caa att gag cgc ctg gct aat cta aag ctt aaa Val Ile Leu Met Gln Gln Ile Glu Arg Leu Ala Asn Leu Lys Leu Lys 120 125 130 135	438
ggc ctt ttt gct tct gaa cta gaa ttt aat ctt ttc aac gaa act tat Gly Leu Phe Ala Ser Glu Leu Glu Phe Asn Leu Phe Asn Glu Thr Tyr 140 145 150	486
aag agt gcc agc caa aag cat tgg aaa aat tta aaa acc gcg cag cct Lys Ser Ala Ser Gln Lys His Trp Lys Asn Leu Lys Thr Ala Gln Pro 155 160 165	534
cat cat caa tgg atg aat att agt gca agt agt ggg att gaa act ttt His His Gln Trp Met Asn Ile Ser Ala Ser Ser Gly Ile Glu Thr Phe 170 175 180	582
atg cgt tct gtg cgt aat aaa tta gaa gaa gcc ggt att ttg atg gag Met Arg Ser Val Arg Asn Lys Leu Glu Glu Ala Gly Ile Leu Met Glu 185 190 195	630
gcg aca cat ccc gaa ttt tta cct agt cag cat gaa ctt aat ttt gta Ala Thr His Pro Glu Phe Leu Pro Ser Gln His Glu Leu Asn Phe Val 200 205 210 215	678
cca gcc gat cct cta aca atg gca gat cgt cat att att gca aaa cat Pro Ala Asp Pro Leu Thr Met Ala Asp Arg His Ile Ile Ala Lys His 220 225 230	726
gga gtt cgc gaa atg gca gaa cag tct gga atg gtt gca act ttt atg Gly Val Arg Glu Met Ala Glu Gln Ser Gly Met Val Ala Thr Phe Met 235 240 245	774
gct aaa ttg agt tca act gcg ctt ggt aat gcc tgc cat att cat atg Ala Lys Leu Ser Ser Thr Ala Leu Gly Asn Ala Cys His Ile His Met 250 255 260	822
tca ctt caa gat gca gaa aca gaa aaa aat gca ttt tat gat caa aac Ser Leu Gln Asp Ala Glu Thr Glu Lys Asn Ala Phe Tyr Asp Gln Asn 265 270 275	870
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 Trp Ala Ile Asp Asn Arg Thr Ser Ala Phe Arg Leu Cys Asn Ser Lys
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tcc gag gga att aat gtt gag ctg cgt att ggt ggc gct gat ttg aac 1110
 Ser Glu Gly Ile Asn Val Glu Leu Arg Ile Gly Gly Ala Asp Leu Asn
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cct tat tta gct ttt tcc gca atc ata gct gca gga att agc ggt ata 1158
 Pro Tyr Leu Ala Phe Ser Ala Ile Ile Ala Ala Gly Ile Ser Gly Ile
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gaa gaa aag ctt gaa ctt ccc cct cct gca tct ggc aat gtt tac aat 1206
 Glu Glu Lys Leu Glu Leu Pro Pro Pro Ala Ser Gly Asn Val Tyr Asn
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gat aag gaa tta cct gaa ttt cct aat tcc tta caa aat gct aca cat 1254
 Asp Lys Glu Leu Pro Glu Phe Pro Asn Ser Leu Gln Asn Ala Thr His
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ctt cta aaa gaa tcg aaa atg ctg aat aaa aca ttc ggg gag aag ttg 1302
 Leu Leu Lys Glu Ser Lys Met Leu Asn Lys Thr Phe Gly Glu Lys Leu
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att cta cat tat gta aac gct gct aat gtt gag att aat gaa ttt tca 1350
 Ile Leu His Tyr Val Asn Ala Ala Asn Val Glu Ile Asn Glu Phe Ser
 425 430 435

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 Lys Gln Val Thr Asp Trp Glu Leu Asn Gln Gly Phe Asn Arg Tyr
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<212> PRT

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Gly Lys Arg Leu Thr Gly Arg His Phe Leu Gly Leu Asp Gln Lys Lys
 35 40 45

Ile Ser Ile Ser Thr Phe Val Tyr Ala Val Thr Ile Glu Gly Ile Ala
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Gly Gly Gly Tyr Glu Ile Ser Ser Val Asp Thr Gly Tyr Ser Asp Cys
 65 70 75 80

His Leu Cys Ala Asp Leu Asn Ser Leu His Leu Leu Pro Trp Ser Glu
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Gly Ala Val Leu Ala Ile Ser Asn Pro His Asn Phe Val Thr Ser Glu
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Pro Leu Phe Cys Ser Pro Arg Val Ile Leu Met Gln Gln Ile Glu Arg
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Leu Ala Asn Leu Lys Leu Lys Gly Leu Phe Ala Ser Glu Leu Glu Phe
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 Ser Ser Gly Ile Glu Thr Phe Met Arg Ser Val Arg Asn Lys Leu Glu
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 Glu Ala Gly Ile Leu Met Glu Ala Thr His Pro Glu Phe Leu Pro Ser
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 Gln His Glu Leu Asn Phe Val Pro Ala Asp Pro Leu Thr Met Ala Asp
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 Arg His Ile Ile Ala Lys His Gly Val Arg Glu Met Ala Glu Gln Ser
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 Gly Met Val Ala Thr Phe Met Ala Lys Leu Ser Ser Thr Ala Leu Gly
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 Ala Ala Gly Ile Ser Gly Ile Glu Glu Lys Leu Glu Leu Pro Pro Pro
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 Ala Ser Gly Asn Val Tyr Asn Asp Lys Glu Leu Pro Glu Phe Pro Asn
 385 390 395 400
 Ser Leu Gln Asn Ala Thr His Leu Leu Lys Glu Ser Lys Met Leu Asn
 405 410 415
 Lys Thr Phe Gly Glu Lys Leu Ile Leu His Tyr Val Asn Ala Ala Asn
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catctctgtg	cagatttgaa	ttcccttcat	ttactcccgt	ggtcagaagg	cgctgtattg	300
gcaatttcca	atcctcataa	tttcgttact	tctgagccat	tgttctgttc	tcctcgagta	360
atactcatgc	agcaaattga	gcgcctggct	aatctaaagc	ttaaaggcct	ttttgcttct	420
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acaatggcag atcgatcatat tattgcaaaa catggaggtt gcgaaatggc agaacagtct 720
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tccttacaaa atgctacaca tcttctaaaa gaatcgaaaa tgctgaataa aacattcg 1260
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 35          40          45
Asp Asp Ile Ala Thr Arg Gly Val Glu Cys Cys Ser Tyr Leu Leu Ala
 50          55          60
Val Asp Val Asp Leu Asn Thr Val Pro Gly Tyr Ala Met Ala Ser Trp
 65          70          75          80
Asp Thr Gly Tyr Gly Asp Met Val Met Thr Pro Asp Leu Ser Thr Leu
 85          90          95
Arg Leu Ile Pro Trp Leu Pro Gly Thr Ala Leu Val Ile Ala Asp Leu
100          105          110
Val Trp Ala Asp Gly Ser Glu Val Ala Val Ser Pro Arg Ser Ile Leu
115          120          125
Arg Arg Gln Leu Asp Arg Leu Lys Ala Arg Gly Leu Val Ala Asp Val
130          135          140
Ala Thr Glu Leu Glu Phe Ile Val Phe Asp Gln Pro Tyr Arg Gln Ala
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Trp Ala Ser Gly Tyr Arg Gly Leu Thr Pro Ala Ser Asp Tyr Asn Ile
165          170          175
Asp Tyr Ala Ile Leu Ala Ser Ser Arg Met Glu Pro Leu Leu Arg Asp
180          185          190
Ile Arg Leu Gly Met Ala Gly Ala Gly Leu Arg Phe Glu Ala Val Lys
195          200          205
Gly Glu Cys Asn Met Gly Gln Gln Glu Ile Gly Phe Arg Tyr Asp Glu
210          215          220
Ala Leu Val Thr Cys Asp Asn His Ala Ile Tyr Lys Asn Gly Ala Lys
225          230          235          240
Glu Ile Ala Asp Gln His Gly Lys Ser Leu Thr Phe Met Ala Lys Tyr
245          250          255
Asp Glu Arg Glu Gly Asn Ser Cys His Ile His Val Ser Leu Arg Gly
260          265          270

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Thr Asp Gly Ser Ala Val Phe Ala Asp Ser Asn Gly Pro His Gly Met
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 305 310 315 320
 Ala Asp Ser Ser Phe Ala Pro Thr Ala Leu Ala Trp Gly Leu Asp Asn
 325 330 335
 Arg Thr Cys Ala Leu Arg Val Val Gly His Gly Gln Asn Ile Arg Val
 340 345 350
 Glu Cys Arg Val Pro Gly Gly Asp Val Asn Gln Tyr Leu Ala Val Ala
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 Ala Leu Ile Ala Gly Gly Leu Tyr Gly Ile Glu Arg Gly Leu Gln Leu
 370 375 380
 Pro Glu Pro Cys Val Gly Asn Ala Tyr Gln Gly Ala Asp Val Glu Arg
 385 390 395 400
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 405 410 415
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